09/623035
PCT/GB99/00582

Lane	1	2	3	4	5	6	7	8
Biotinylation	+	+	+	+	+	+	+	+
791T/36	+	-	+	-	+	-	+	-
1143/B7	-	+	-	+	-	+	-	+
DTSSP	-	-	+	+	-	-	+	+
Solublisation	x	x	x	x	o	o	o	o

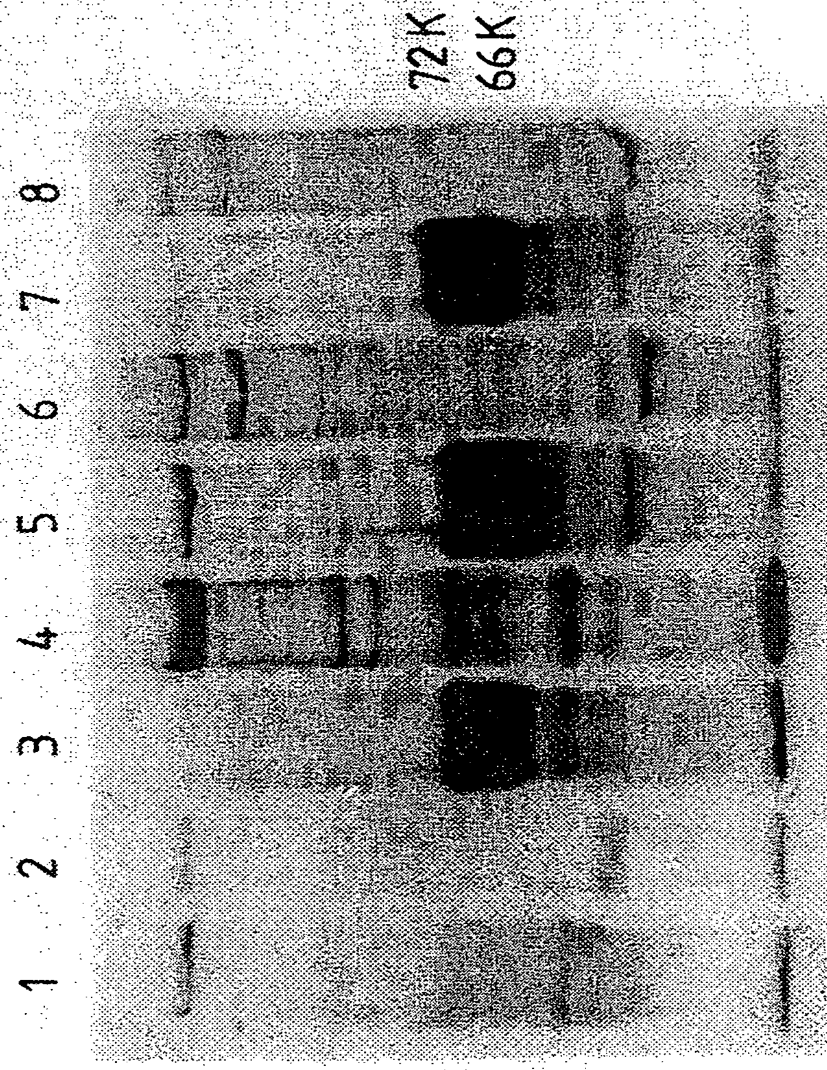

Fig. 1

Detergent						
Glucoside	+	-	-	-	-	-
NP-40	-	+	-	-	-	-
TX-100	-	-	+	+	+	+
Centrifugation						
13000 rpm	+	+	+	+	+	+
100, 000 g	+	+	+	-	+	+
blue-2	-	-	-	-	+	+

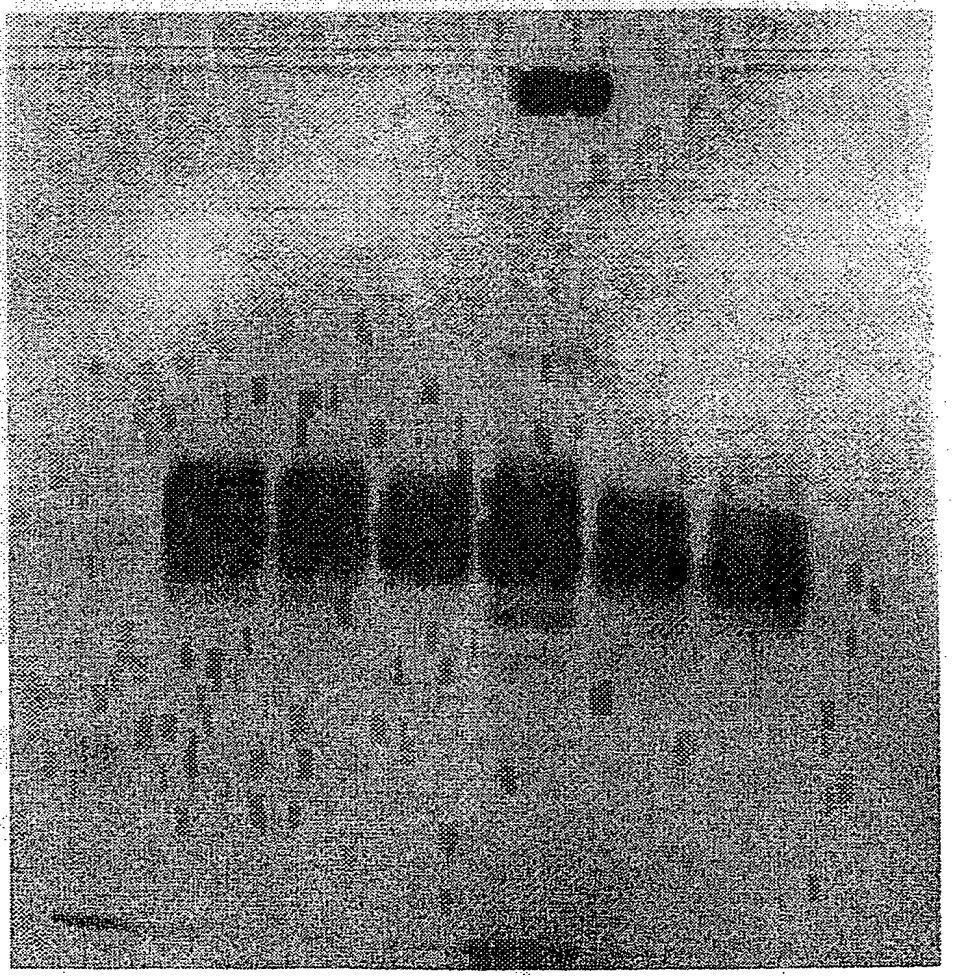

Fig. 2

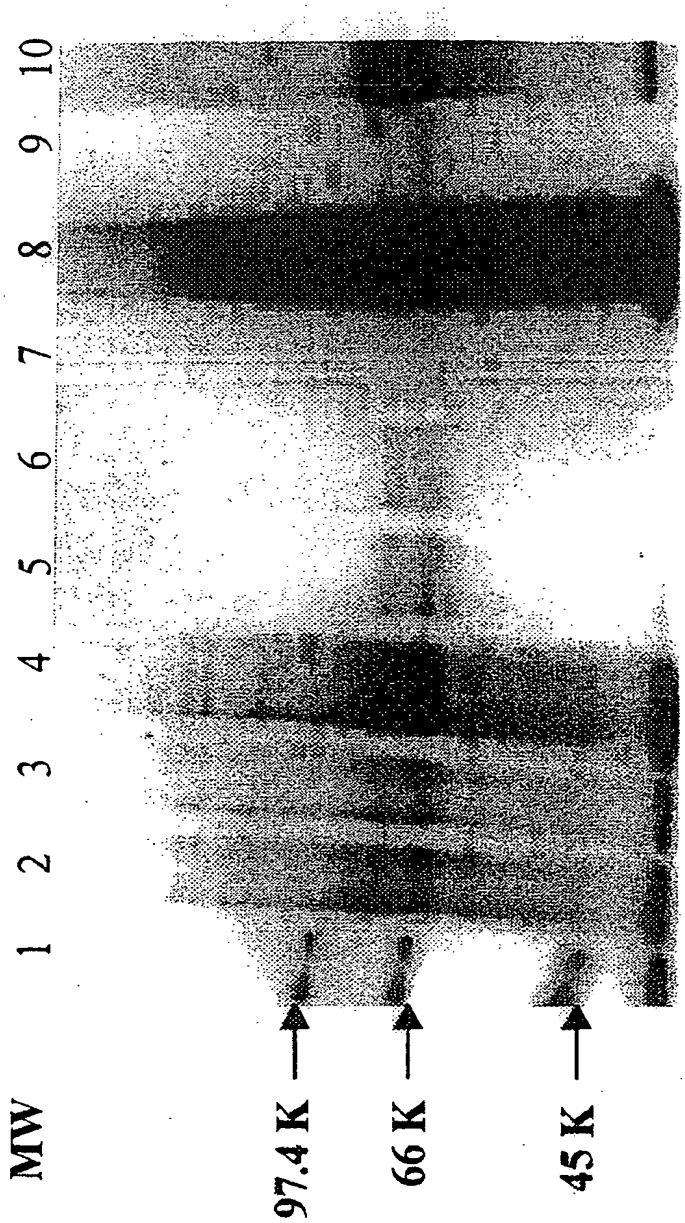

Fig. 3

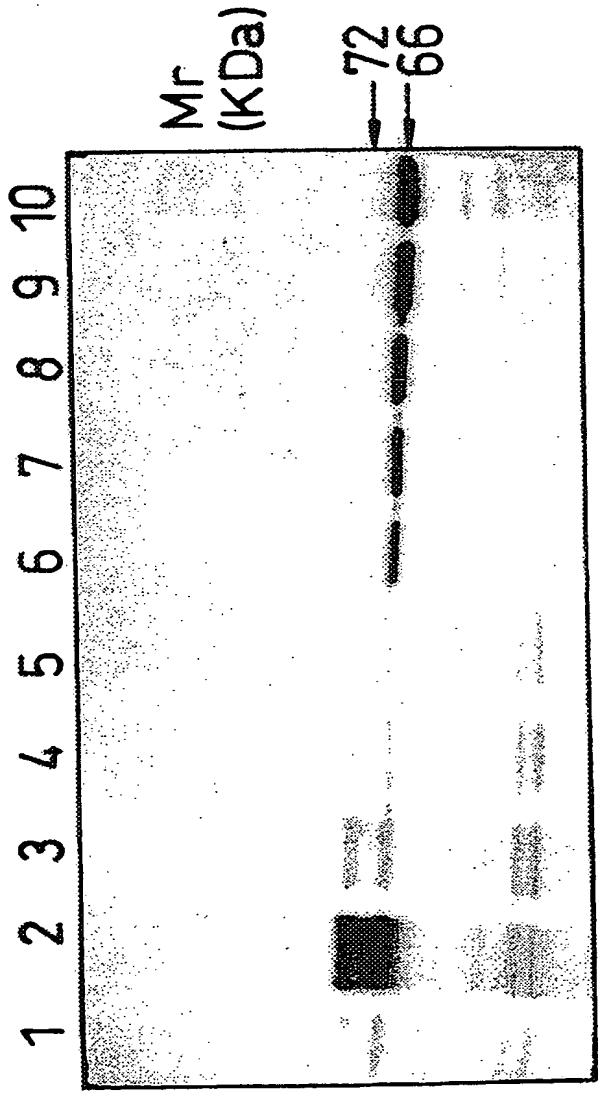

Fig. 4

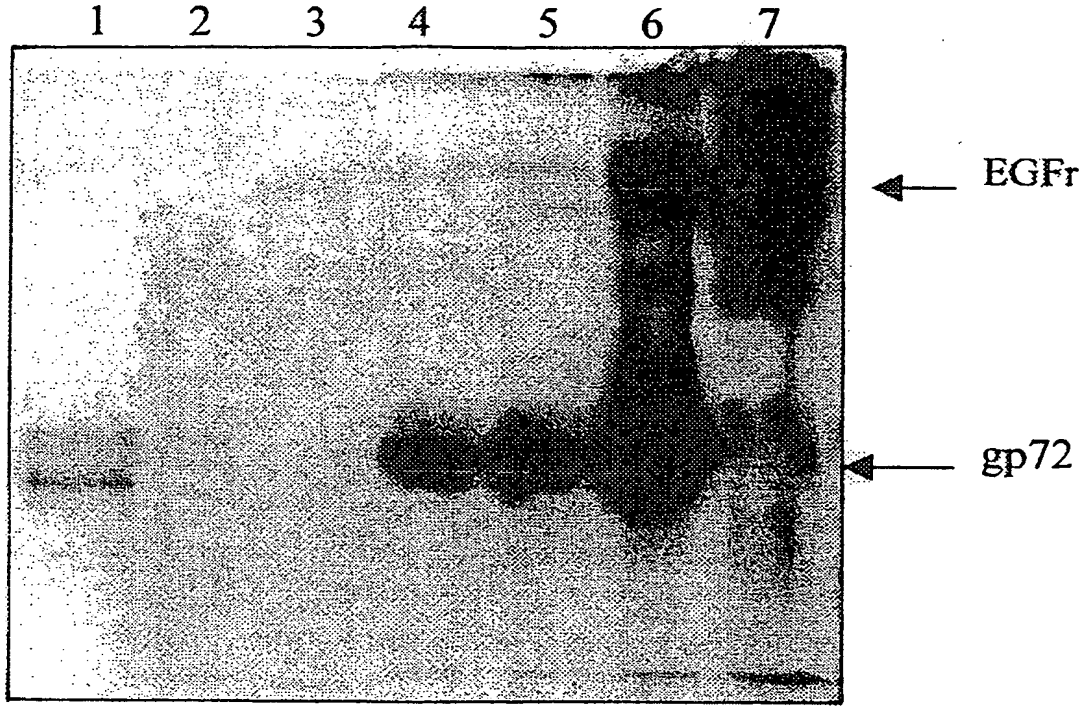

Fig. 5

09/623035

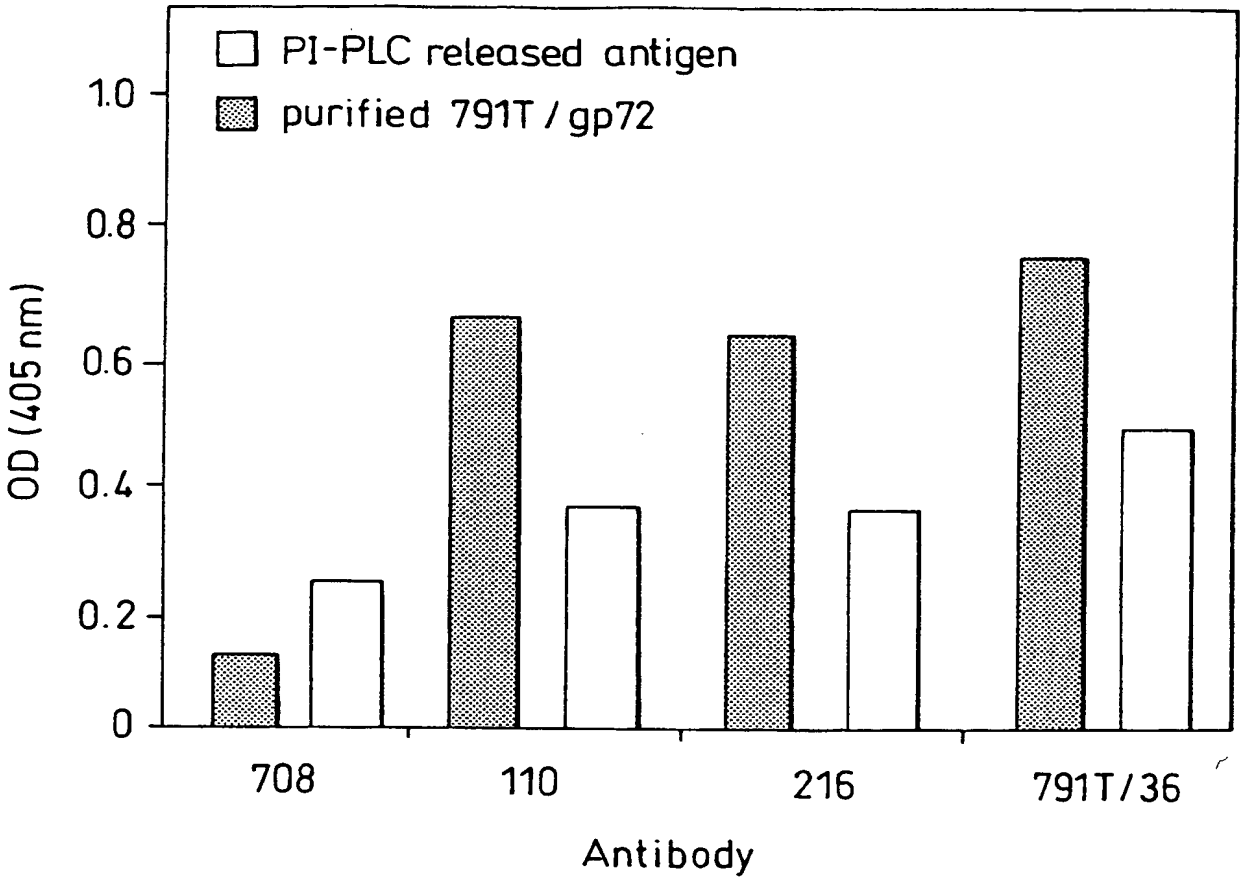

Fig. 6

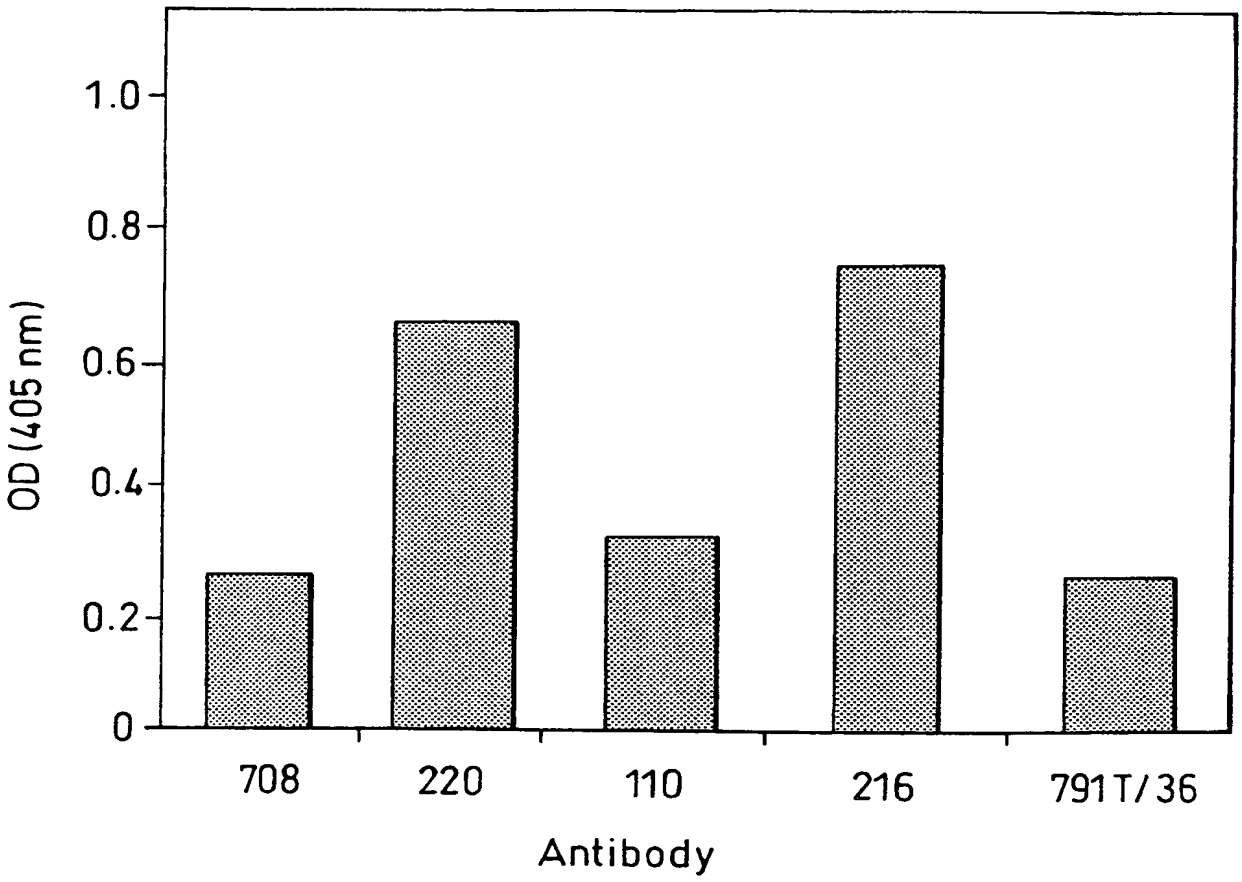

Fig. 7

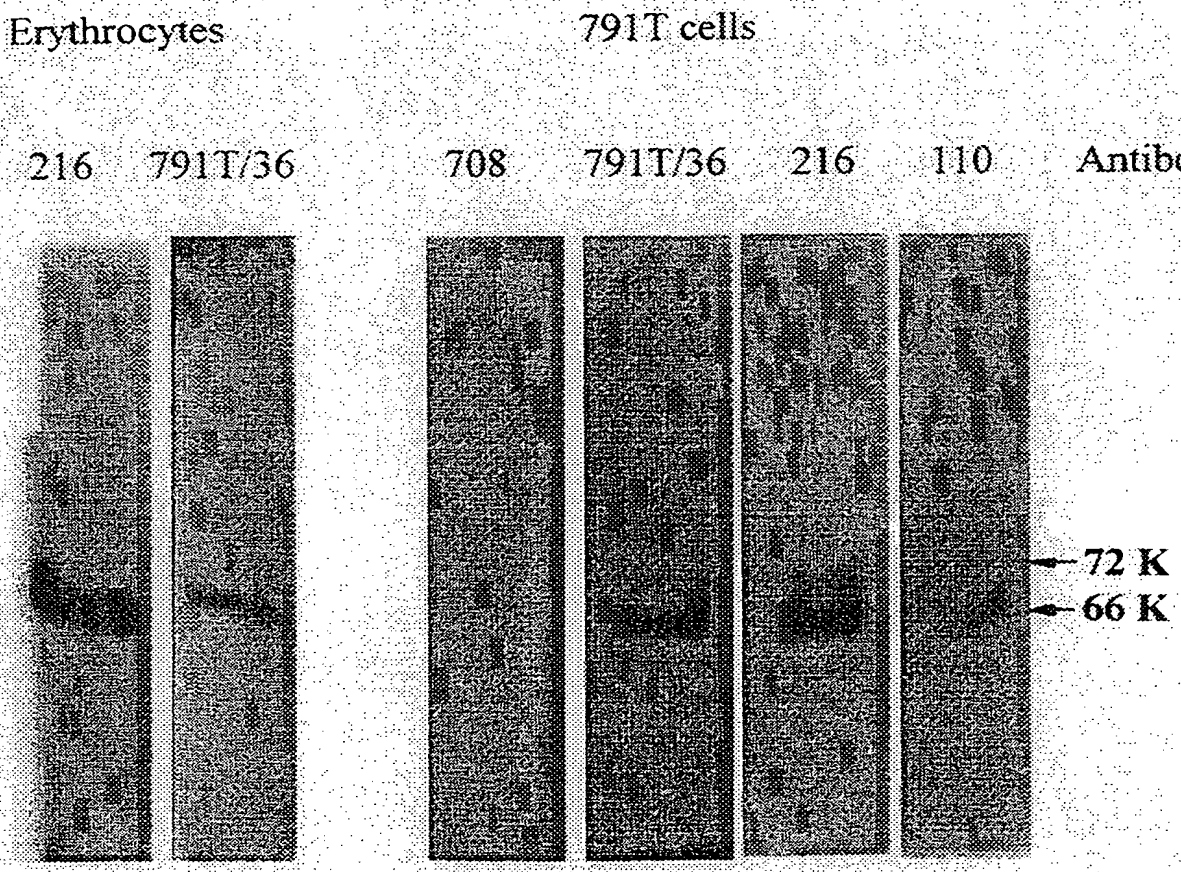

Fig. 8

09/623035 19 OCT 2000

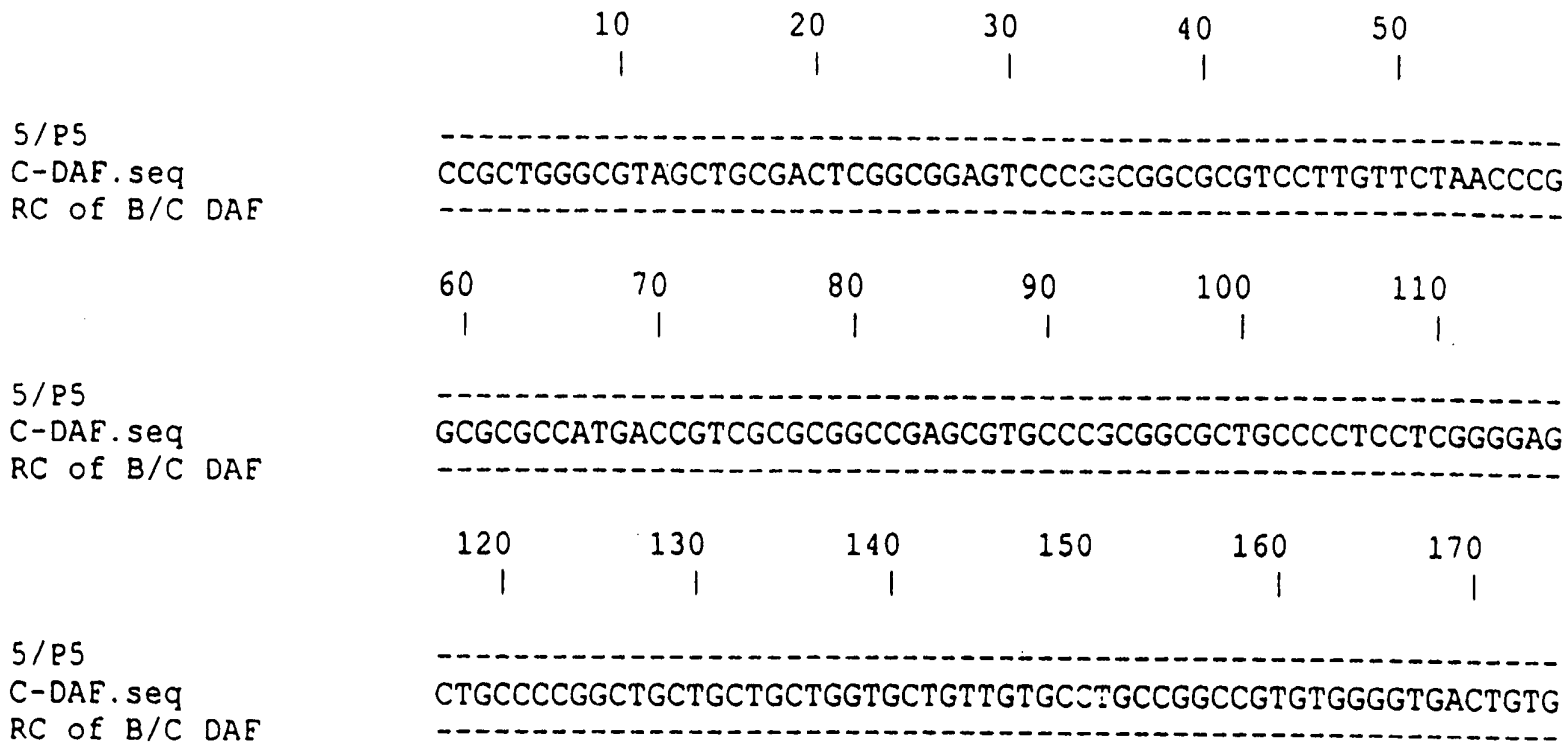

Fig. 9 (part 1 of 11)

SUBSTITUTE SHEET (RULE 26)

```
                    180        190        200        210        220        230
                     |          |          |          |          |          |
5/P5                ------------------------------------------GTACAAGTTTTCC
C-DAF.seq           GCCTTCCCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCC
RC of B/C DAF       ------------------------------------------------------------

                    240        250        260        270        280        290
                     |          |          |          |          |          |
5/P5                CGAGGATACTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAG
C-DAF.seq           CGAGGATACTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAG
RC of B/C DAF       ------------------------------------------------------------

                    300        310        320        330        340
                     |          |          |          |          |
5/P5                AAGGACTCAGTGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCA
C-DAF.seq           AAGGACTCAGTGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCA
RC of B/C DAF       ------------------------------------------------------------
```

Fig. 9 (part 2 of 11)

SUBSTITUTE SHEET (RULE 26)

```
                    350        360        370        380        390        400
                     |          |          |          |          |          |
5/P5                ATCGTAGCTGCGAGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATAT
C-DAF.seq           ATCGTAGCTGCGAGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATAT
RC of B/C DAF       ------------------------------------------------------------

                    410        420        430        440        450        460
                     |          |          |          |          |          |
5/P5                CACTCAGAATTATTTTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTAC
C-DAF.seq           CACTCAGAATTATTTTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTAC
RC of B/C DAF       ------------------------------------------------------------

                    470        480        490        500        510        520
                     |          |          |          |          |          |
5/P5                AGAAGAGAACCTTCTCTATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCA
C-DAF.seq           AGAAGAGAACCTTCTCTATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCA
RC of B/C DAF       ------------------------------------------------------------

                    530        540        550        560        570        580
                     |          |          |          |          |          |
5/P5                CAGCAGTCGAATTTTGTAAAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGG
C-DAF.seq           CAGCAGTCGAATTTTGTAAAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGG
RC of B/C DAF       ------------------------------------------------------------
```

Fig. 9 (part 3 of 11)

PCT/GB99/00582

SUBSTITUTE SHEET (RULE 26)

```
                                590         600         610         620         630
                                 |           |           |           |           |
5/P5                    TCAGATTGATGTACCAGGTGGCATATTATTTGATGCAACCATCTCCTTCTCATGTAA
C-DAF.seq               TCAGATTGATGTACCAGGTGGCATATTATTTGGTGCAACCATCTCCTTCTCATGTAA
RC of B/C DAF           ----------------------TATTATTTGNTGCAACCATTTCCTTTTCATGTAA

                       640         650         660         670         680         690
                        |           |           |           |           |           |
5/P5                    CACAGGGGTACAAATTATTTGGCTCGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTC
C-DAF.seq               CACAGGG-TACAAATTATTTGGCTCGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTC
RC of B/C DAF           CACANGG-TACAAATTATTTGGCTCGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTC

                        700         710         720         730         740         750
                         |           |           |           |           |           |
5/P5                    TGTCCAGTGGAGTGACCCGTTGCCAGAATGCAGAGAAATTTA-TGTCCAGCACCACCA
C-DAF.seq               TGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAATTTATTGTCCAGCACCACCA
RC of B/C DAF           TGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAATTTATTGTCCAGCACCACCA
```

Fig. 9 (part 4 of 11)

SUBSTITUTE SHEET (RULE 26)

```
                    760        770        780        790        800        810
                     |          |          |          |          |          |
5/P5                CAAATTGACA-TGGAATAATCCAGGGGAACGTTGACCATTATGGATATAAACG-----
C-DAF.seq           CAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATTATGGATATAGACAGTCTG
RC of B/C DAF       CAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATTATGGATATAGACAGTCTG

                         820        830        840        850        860        870
                          |          |          |          |          |          |
5/P5                ------------------------------------------------------------
C-DAF.seq           TAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGCACTCTATTTATTGTAC
RC of B/C DAF       TAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGCACTCTATTTATTGTAC

                               880        890        900        910        920
                                |          |          |          |          |
5/P5                ------------------------------------------------------------
C-DAF.seq           TGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAATGCAGAGGAAAATCT
RC of B/C DAF       TGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAATGCAGAGGAAAATCT
```

Fig. 9 (part 5 of 11)

SUBSTITUTE SHEET (RULE 26)

```
                  930        940        950        960        970        980
                   |          |          |          |          |          |
5/P5              ------------------------------------------------------------
C-DAF.seq         CTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAAATGTTCCAACTA
RC of B/C DAF     CTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAAATGTTCCAACTA

                  990       1000       1010       1020       1030       1040
                   |          |          |          |          |          |
5/P5              ------------------------------------------------------------
C-DAF.seq         CAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACACCAAATGCTCA
RC of B/C DAF     CAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACACCAAATGCTCA

                 1050       1060       1070       1080       1090       1100
                   |          |          |          |          |          |
5/P5              ------------------------------------------------------------
C-DAF.seq         AGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAACAACCCCA
RC of B/C DAF     AGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAACAACCCCA

                 1110       1120       1130       1140       1150       1160
                   |          |          |          |          |          |
5/P5              ------------------------------------------------------------
C-DAF.seq         AATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTGTT
RC of B/C DAF     AATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTGTT
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Fig. 9 (part 6 of 11)

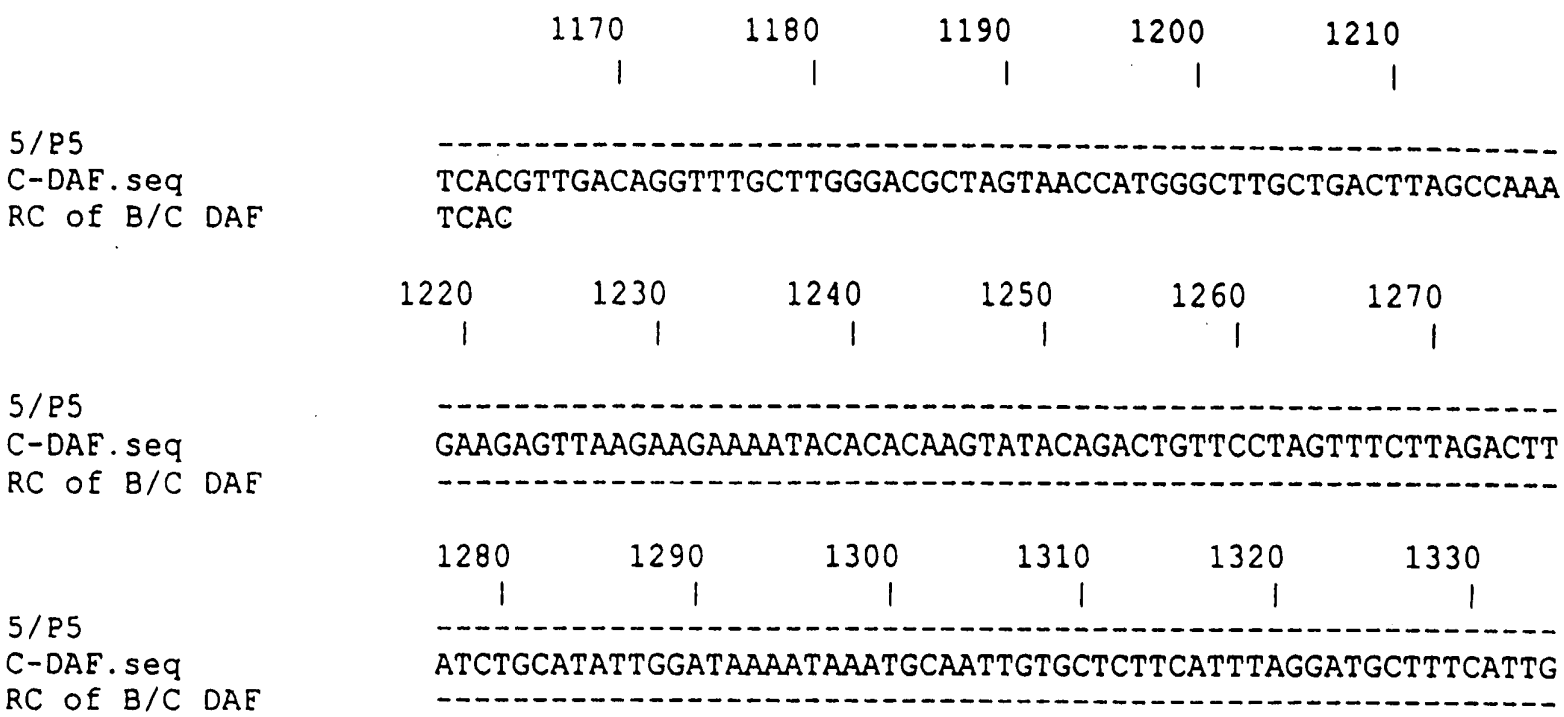

Fig. 9 (part 7 of 11)

SUBSTITUTE SHEET (RULE 26)

09623035 . 010201

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                           1340      1350      1360      1370      1380      1390
                              |         |         |         |         |         |
5/P5               -----------------------------------------------------------
C-DAF.seq          TCTTTAAGATGTGTTAGGAATGTCAACAGAGCAAGGAGAAAAAAGGCAGTCCTGGAAT
RC of B/C DAF      -----------------------------------------------------------

                            1400      1410      1420      1430      1440      1450
                               |         |         |         |         |         |
5/P5               -----------------------------------------------------------
C-DAF.seq          CACATTCTTAGCACACCTACACCTCTTGAAAATAGAACAACTTGCAGAATTGAGAGTG
RC of B/C DAF      -----------------------------------------------------------

                             1460      1470      1480      1490      1500
                                |         |         |         |         |
5/P5               -----------------------------------------------------------
C-DAF.seq          ATTCCTTTCCTAAAAGTGTAAGAAAGCATAGAGATTTGTTCGTATTTAGAATGGGATC
RC of B/C DAF      -----------------------------------------------------------
```

Fig. 9 (part 8 of 11)

00210T" SE0E2960

```
                  1510      1520      1530      1540      1550      1560
                     |         |         |         |         |         |
5/P5              ----------------------------------------------------------
C-DAF.seq         ACGAGGAAAAGAGAAGGAAAGTGATTTTTTTCCACAAGATCTGTAATGTTATTTCCAC
RC of B/C DAF     ----------------------------------------------------------

                    1570      1580      1590      1600      1610      1620
                       |         |         |         |         |         |
5/P5              ----------------------------------------------------------
C-DAF.seq         TTATAAAGGAAATAAAAAATGAAAAACATTATTTGGATATCAAAAGCAAATAAAAACC
RC of B/C DAF     ----------------------------------------------------------

                      1630      1640      1650      1660      1670      1680
                         |         |         |         |         |         |
5/P5              ----------------------------------------------------------
C-DAF.seq         CAATTCAGTCTCTTCTAAGCAAAATTGCTAAAGAGAGATGAACCACATTATAAAGTAA
RC of B/C DAF     ----------------------------------------------------------

                        1690      1700      1710      1720      1730      1740
                           |         |         |         |         |         |
5/P5              ----------------------------------------------------------
C-DAF.seq         TCTTTGGCTGTAAGGCATTTTCATCTTTCCTTCGGGTTGGCAAAATATTTTAAAGGTA
RC of B/C DAF     ----------------------------------------------------------
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Fig. 9 (part 9 of 11)

SUBSTITUTE SHEET (RULE 26)

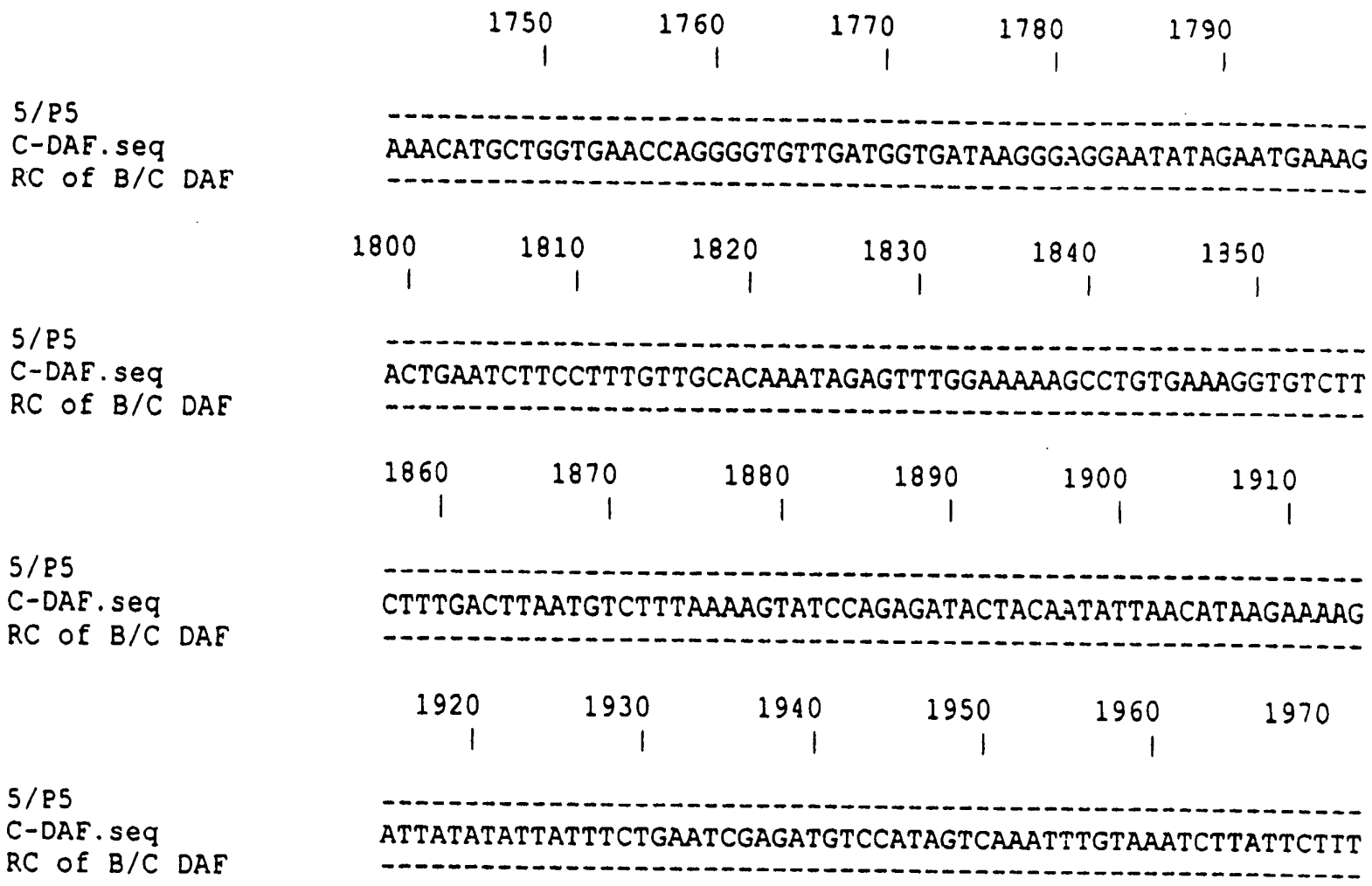

Fig. 9 (part 10 of 11)

SUBSTITUTE SHEET (RULE 26)

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5/P5                      ------------------------------------------------------------
C-DAF.seq                 TGTAATATTTATTTATATTTATTTATGACAGTGAACATTCTGATTTTACATGTAAAAC
RC of B/C DAF             ------------------------------------------------------------

                             2040      2050      2060      2070      2080
                               |         |         |         |         |
5/P5                      ------------------------------------------------------------
C-DAF.seq                 AAGAAAAGTTGAAGAAGATATGTGAAGAAAAATGTATTTTTCCTAAATAGAAATAAAT
RC of B/C DAF             ------------------------------------------------------------

                        2090      2100
                          |         |
5/P5                      ---------------T
C-DAF.seq                 GATCCCATTTTTTGGT
RC of B/C DAF             ----------------
```

Fig. 9 (part 11 of 11)

```
1                                                                  CC GCT GGG CGT AGC

15   TGC GAC TCG GCG GAG TCC CGG CGG CGC GTC CTT GTT CTA ACC CGG CGC GCC
     |<-- Leader sequence
     Met Thr Val Ala Arg Pro Ser Val Pro Ala Ala Leu Pro Leu Leu Gly Glu  17
66   ATG ACC GTC GCG CGG CCG AGC GTG CCC GCG GCG CTG CCC CTC CTC GGG GAG

     Leu Pro Arg Leu Leu Leu Leu Val Leu Leu Cys Leu Pro Ala Val Trp Gly  34
117  CTG CCC CGG CTG CTG CTG CTG GTG CTG TTG TGC CTG CCG GCC GTG TGG GGT
      <- sushi 1
     |<-- mature sequence (first 16 amino acids sequenced)
     Asp Cys Gly Leu Pro Pro Asp Val Pro Asn Ala Gln Pro Ala Leu Glu Gly  51
168  GAC TGT GGC CTT CCC CCA GAT GTA CCT AAT GCC CAG CCA GCT TTG GAA GGC

     Arg Thr Ser Phe Pro Glu Asp Thr Val Ile Thr Tyr Lys Cys Glu Glu Ser  68
219  CGT ACA AGT TTT CCC GAG GAT ACT GTA ATA ACG TAC AAA TGT GAA GAA AGC

     Phe Val Lys Ile Pro Gly Glu Lys Asp Ser Val Ile Cys Leu Lys Gly Ser  85
270  TTT GTG AAA ATT CCT GGC GAG AAG GAC TCA GTG ATC TGC CTT AAG GGC AGT
                                    sushi 1 ->|    |sushi 2
     Gln Trp Ser Asp Ile Glu Glu Phe Cys Asn Arg Ser Cys Glu Val Pro Thr 102
321  CAA TGG TCA GAT ATT GAA GAG TTC TGC AAT CGT AGC TGC GAG GTG CCA ACA

     Arg Leu Asn Ser Ala Ser Leu Lys Gln Pro Tyr Ile Thr Gln Asn Tyr Phe 119
372  AGG CTA AAT TCT GCA TCC CTC AAA CAG CCT TAT ATC ACT CAG AAT TAT TTT

     Pro Val Gly Thr Val Val Glu Tyr Glu Cys Arg Pro Gly Tyr Arg Arg Glu 136
423  CCA GTC GGT ACT GTT GTG GAA TAT GAG TGC CGT CCA GGT TAC AGA AGA GAA

     Pro Ser Leu Ser Pro Lys Leu Thr Cys Leu Gln Asn Leu Lys Trp Ser Thr 153
474  CCT TCT CTA TCA CCA AAA CTA ACT TGC CTT CAG AAT TTA AAA TGG TCC ACA
                    sushi 2->|         |<- sushi 3
     Ala Val Glu Phe Cys Lys Lys Lys Ser Cys Pro Asn Pro Gly Glu Ile Arg 170
525  GCA GTC GAA TTT TGT AAA AAG AAA TCA TGC CCT AAT CCG GGA GAA ATA CGA

     Asn Gly Gln Ile Asp Val Pro Gly Gly Ile Leu Phe Gly Ala Thr Ile Ser 187
576  AAT GGT CAG ATT GAT GTA CCA GGT GGC ATA TTA TTT GGT GCA ACC ATC TCC

     Phe Ser Cys Asn Thr Gly Tyr Lys Leu Phe Gly Ser Thr Ser Ser Phe Cys 204
627  TTC TCA TGT AAC ACA GGG TAC AAA TTA TTT GGC TCG ACT TCT AGT TTT TGT
                                                          sushi 3 ->|
     Leu Ile Ser Gly Ser Ser Val Gln Trp Ser Asp Pro Leu Pro Glu Cys Arg 221
678  CTT ATT TCA GGC AGC TCT GTC CAG TGG AGT GAC CCG TTG CCA GAG TGC AGA
           |<- sushi 4
     Glu Ile Tyr Cys Pro Ala Pro Pro Gln Ile Asp Asn Gly Ile Ile Gln Gly 238
729  GAA ATT TAT TGT CCA GCA CCA CCA CAA ATT GAC AAT GGA ATA ATT CAA GGG
```

Fig. 10 (part 1 of 2)

```
     Glu Arg Asp His Tyr Gly Tyr Arg Gln Ser Val Thr Tyr Ala Cys Asn Lys 255
780  GAA CGT GAC CAT TAT GGA TAT AGA CAG TCT GTA ACG TAT GCA TGT AAT AAA

     Gly Phe Thr Met Ile Gly Glu His Ser Ile Tyr Cys Thr Val Asn Asn Asp 272
831  GGA TTC ACC ATG ATT GGA GAG CAC TCT ATT TAT TGT ACT GTG AAT AAT GAT
                                        sushi 4->|
     Glu Gly Glu Trp Ser Gly Pro Pro Pro Glu Cys Arg Gly Lys Ser Leu Thr 289
885  GAA GGA GAG TGG AGT GGC CCA CCA CCT GAA TGC AGA GGA AAA TCT CTA ACT

     Ser Lys Val Pro Pro Thr Val Gln Lys Pro Thr Thr Val Asn Val Pro Thr 306
933  TCC AAG GTC CCA CCA ACA GTT CAG AAA CCT ACC ACA GTA AAT GTT CCA ACT

     Thr Glu Val Ser Pro Thr Ser Gln Lys Thr Thr Thr Lys Thr Thr Thr Pro 323
984  ACA GAA GTC TCA CCA ACT TCT CAG AAA ACC ACC ACA AAA ACC ACC ACA CCA

     Asn Ala Gln Ala Thr Arg Ser Thr Pro Val Ser Arg Thr Thr Lys His Phe 340
1035 AAT GCT CAA GCA ACA CGG AGT ACA CCT GTT TCC AGG ACA ACC AAG CAT TTT

     His Glu Thr Thr Pro Asn Lys Gly Ser Gly Thr Thr Ser Gly Thr Thr Arg 357
1086 CAT GAA ACA ACC CCA AAT AAA GGA AGT GGA ACC ACT TCA GGT ACT ACC CGT

     Leu Leu Ser Gly His Thr Cys Phe Thr Leu Thr Gly Leu Leu Gly Thr Leu 374
1137 CTT CTA TCT GGG CAC ACG TGT TTC ACG TTG ACA GGT TTG CTT GGG ACG CTA

     Val Thr Met Gly Leu Leu Thr Stop                                    381
1188 GTA ACC ATG GGC TTG CTG ACT TAG CCAAAGAAGAGTTAAGAAG

1231 AAAATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGACTTATCTGCATATTGGATAAAATAAA
1298 TGCAATTGTGCTCTTCATTTAGGATGCTTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACAGAGC
1365 AAGGAGAAAAAAGGCAGTCCTGGAATCACATTCTTAGCACACCTACACCTCTTGAAAATAGAACAAC
1432 TTGCAGAATTGAGAGTGATTCCTTTCCTAAAAGTGTAAGAAAGCATAGAGATTTGTTCGTATTTAGA
1499 ATGGGATCACGAGGAAAAGAGAAGGAAAGTGATTTTTTTCCACAAGATCTGTAATGTTATTTCCACT
1566 TATAAAGGAAATAAAAAATGAAAAACATTATTTGGATATCAAAAGCAAATAAAAACCCAATTCAGTC
1633 TCTTCTAAGCAAAATTGCTAAAGAGAGATGAACCACATTATAAAGTAATCTTTGGCTGTAAGGCATT
1700 TTCATCTTTCCTTCGGGTTGGCAAAATATTTTAAAGGTAAAACATGCTGGTGAACCAGGGGTGTTGA
1767 TGGTGATAAGGGAGGAATATAGAATGAAAGACTGAATCTTCCTTTGTTGCACAAATAGAGTTTGGAA
1834 AAAGCCTGTGAAAGGTGTCTTCTTTGACTTAATGTCTTTAAAAGTATCCAGAGATACTACAATATTA
1901 ACATAAGAAAAGATTATATATTATTTCTGAATCGAGATGTCCATAGTCAAATTTGTAAATCTTATTC
1968 TTTTGTAATATTTATTTATATTTATTTATGACAGTGAACATTCTGATTTTACATGTAAAACAAGAAA
2035 AGTTGAAGAAGATATGTGAAGAAAAATGTATTTTTCCTAAATAGAAATAAATGATCCCATTTTTTGG
2102 T
```

Fig. 10 (part 2 of 2)

```
  1    TTTAAACGGGCCCTCTAGACTCGAGCGGCCGCTGCCCATCTTGTCGTCGTCGTCCTTGTAGTCG
 65 TGCATGTGGTGGTGGTGGTGGTGGTTAACCATGGTGGCGGGCCGCCACTGTGCTGGATATCTGCAGA
132 ATTCGATGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCC

    Met Thr Val Ala Arg Pro Ser Val Pro Ala Ala Leu Pro Leu Leu Gly Glu  17
199 ATG ACC GTC GCG CGG CCG AGC GTG CCC GCG GCG CTG CCC CTC CTC GGG GAG

    Leu Pro Arg Leu Leu Leu Leu Val Leu Leu Cys Leu Pro Ala Val Trp Gly  34
250 CTG CCC CGG CTG CTG CTG CTG GTG CTG TTG TGC CTG CCG GCC GTG TGG GGT

    Asp Cys Gly Leu Pro Pro Asp Val Pro Asn Ala Gln Pro Ala Leu Glu Gly  51
301 GAC TGT GGC CTT CCC CCA GAT GTA CCT AAT GCC CAG CCA GCT TTG GAA GGC

    Arg Thr Ser Phe Pro Glu Asp Thr Val Ile Thr Tyr Lys Cys Glu Glu Ser  68
352 CGT ACA AGT TTT CCC GAG GAT ACT GTA ATA ACG TAC AAA TGT GAA GAA AGC

    Phe Val Lys Ile Pro Gly Glu Lys Asp Ser Val Ile Cys Leu Lys Gly Ser  85
403 TTT GTG AAA ATT CCT GGC GAG AAG GAC TCA GTG ATC TGC CTT AAG GGC AGT

    Gln Trp Ser Asp Ile Glu Glu Phe Cys Asn Arg Ser Cys Glu Val Pro Thr 102
454 CAA TGG TCA GAT ATT GAA GAG TTC TGC AAT CGT AGC TGC GAG GTG CCA ACA

    Arg Leu Asn Ser Ala Ser Leu Lys Gln Pro Tyr Ile Thr Gln Asn Tyr Phe 119
505 AGG CTA AAT TCT GCA TCC CTC AAA CAG CCT TAT ATC ACT CAG AAT TAT TTT

    Pro Val Gly Thr Val Val Glu Tyr Glu Cys Arg Pro Gly Tyr Arg Arg Glu 136
556 CCA GTC GGT ACT GTT GTG GAA TAT GAG TGC CGT CCA GGT TAC AGA AGA GAA

    Pro Ser Leu Ser Pro Lys Leu Thr Cys Leu Gln Asn Leu Lys Trp Ser Thr 153
607 CCT TCT CTA TCA CCA AAA CTA ACT TGC CTT CAG AAT TTA AAA TGG TCC ACA

    Ala Val Glu Phe Cys Lys Lys Lys Ser Cys Pro Asn Pro Gly Glu Ile Arg 170
658 GCA GTC GAA TTT TGT AAA AAG AAA TCA TGC CCT AAT CCG GGA GAA ATA CGA

    Asn Gly Gln Ile Asp Val Pro Gly Gly Ile Leu Phe Gly Ala Thr Ile Ser 187
709 AAT GGT CAG ATT GAT GTA CCA GGT GGC ATA TTA TTT GGT GCA ACC ATC TCC

    Phe Ser Cys Asn Thr Gly Tyr Lys Leu Phe Gly Ser Thr Ser Ser Phe Cys 204
760 TTC TCA TGT AAC ACA GGG TAC AAA TTA TTT GGC TCG ACT TCT AGT TTT TGT
```

Fig. 11 (part 1 of 2)

```
    Leu Ile Ser Gly Ser Ser Val Gln Trp Ser Asp Pro Leu Pro Glu Cys Arg 221
811 CTT ATT TCA GGC AGC TCT GTC CAG TGG AGT GAC CCG TTG CCA GAG TGC AGA

    Glu Ile Tyr Cys Pro Ala Pro Pro Gln Ile Asp Asn Gly Ile Ile Gln Gly 238
862 GAA ATT TAT TGT CCA GCA CCA CCA CAA ATT GAC AAT GGA ATA ATT CAA GGG

    Glu Arg Asp His Tyr Gly Tyr Arg Gln Ser Val Thr Tyr Ala Cys Asn Lys 255
913 GAA CGT GAC CAT TAT GGA TAT AGA CAG TCT GTA ACG TAT GCA TGT AAT AAA

    Gly Phe Thr Met Ile Gly Glu His Ser Ile Tyr Cys Thr Val Asn Asn Asp 272
964 GGA TTC ACC ATG ATT GGA GAG CAC TCT ATT TAT TGT ACT GTG AAT AAT GAT

    Glu Gly Glu Trp Ser Gly Pro Pro Pro Glu Cys Arg Gly Lys Ser Leu Thr 289
1015GAA GGA GAG TGG AGT GGC CCA CCA CCT GAA TGC AGA GGA AAA TCT CTA ACT

    Ser Lys Val Pro Pro Thr Val Gln Lys Pro Thr Thr Val Asn Val Pro Thr 306
1066TCC AAG GTC CCA CCA ACA GTT CAG AAA CCT ACC ACA GTA AAT GTT CCA ACT

    Thr Glu Val Ser Pro Thr Ser Gln Lys Thr Thr Thr Lys Thr Thr Thr Pro 323
1117ACA GAA GTC TCA CCA ACT TCT CAG AAA ACC ACC ACA AAA ACC ACC ACA CCA

   Asn Ala Gln Ala Thr Arg Ser Thr Pro Val Ser Arg Thr Thr Lys His Phe 340
1168AAT GCT CAA GCA ACA CGG AGT ACA CCT GTT TCC AGG ACA ACC AAG CAT TTT

    His Glu Thr Thr Pro Asn Lys Gly Ser Gly Thr Thr Ser Gly Thr Thr Arg 357
1219CAT GAA ACA ACC CCA AAT AAA GGA AGT GGA ACC ACT TCA GGT ACT ACC CGT

    Leu Leu Ser Gly His Thr Cys Phe Thr Leu Thr Gly Leu Leu Gly Thr Leu 374
1270CTT CTA TCT GGG CAC ACG TGT TTC ACG TTG ACA GGT TTG CTT GGG ACG CTA

    Val Thr Met Gly Leu Leu Thr Stop                                    381
1321GTA ACC ATG GGC TTG CTG ACT TAG CCAAAGAAGAGTTAAGAAGAAAATACACACAAGTA

1380TACAGACTGTTCCTAGTTTCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTC
1447ATTTAGGATGCTTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACA
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Fig. 11 (part 2 of 2)